

Db 50 GTGTGGAGTAGCTGTATACACCTGTTTATATAGTAGTATCATATAATTAAAC 1

RESULT 5

BG176206 996 bp mRNA EST 06-FEB-2001  
 LOCUS 60233535F2 NC1\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:4458252 5'  
 DEFINITION mRNA sequence.  
 BG176206  
 BG176206.1 GI:12682909  
 EST.  
 house mouse.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus;  
 1 (bases 1 to 996)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs.rem@nih.gov](mailto:cgapbs.rem@nih.gov)  
 Tissue Procurement: Gilbert Smith, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLAM10256 row: f column: 13  
 High quality sequence stop: 668.  
 Location/Qualifiers  
 1. .996  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:4458252"  
 /clone\_lib="NCI\_CGAP\_Mam1"  
 /tissue\_type="tumor, biopsy sample"  
 /dev\_stage="3 months, virgin"  
 /lab\_host="DH10B"  
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt:  
 Site: 2; NotI: Cloned unidirectionally. Primer: Oligo dT:  
 Library constructed by Life Technologies, Inc. Investigator  
 providing samples: Gilbert Smith, NIH"  
 BASE COUNT 294 a 214 c 243 g 244 t 1 others  
 ORIGIN

Query Match 33.5%; Score 718; DB 174; Length 996;  
 Best Local Similarity 96.3%; Pred. No. 6.8e-183;  
 Matches 788; Conservative 0; Mismatches 25; Indels 5; Gaps 5;

QY 865 attgcaattcgaaggaacaaataattctcagctattcacaagaggcatccaagtca 924  
 Db 1 ATTGGCAATCTGAAGGACAAATAATCTCAGTCTATTCAAGAGGCATCCAAGTCACA 60  
 QY 925 atggtcatcgaagttagggaaaaaacatggcccttgggtgaatcattatcaattttctc 984  
 Db 61 ATGGTCATCGAAGTAGGGAAAAAACAATGGCCC-TGGGTGAATCATTTATCAATTTTCTTC 119  
 QY 985 gttctgtctctttttcaataatcaggcaaacgctgggtatttcattctttattct 1044  
 Db 120 GTTCTGTGTCCCTTTTTCATAATTACGGCAGCAACCGTGGGCTATTTCATCTTTATCT 179  
 QY 1045 gctcgaagattacgaatcgaagagctcgaagcaggaagcagaggcagtttaaggcagat 1104  
 Db 180 GCTCGAAGATTACGAATCAAGAGCTCAAAGCAGGAAGCAGAGGCAGTTTAAAGGCAGAT 239  
 QY 1105 gctaaaaagctattggaagcttcagctgcgcaccttgaacaagaggagaagaatt 1164  
 Db 240 GGTAAAAAGCATTCGAAGGCTTCAGCTCGGCACCTTGAACAAGAGGACAGAAGAAAT 299  
 QY 1165 gacctgtatgaatagctctctgtctgtcattgaactctataagccaaatatttggtg 1224

1 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
2 Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,  
3 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pachleb J.M., M.G.,  
4 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese H.,  
5 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
6 Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
7 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
8 Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
9 Wang Z.-Y., Wasserman D.A., Weinstock K.M., Weissbach J.,  
10 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
11 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
12 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
13 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
14 \*The genome sequence of Drosophila melanogaster\*.  
15 Science 287:2185-2195(2000).  
16 - SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.  
17 EMBL: AF003486; AAF47316.1;  
18 FlyBase: FBgn0004919; gcl.  
19 InterPro: IPR001841;  
20 InterPro: IPR003015;  
21 Pfam: PF00097; zf-C3HC4; 1.  
22 PROSITE: PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
23 SMART: SM00184; RING; 1.  
24 Zinc-finger.  
25 SEQUENCE 286 AA; 32183 MW; D7A477D8880C682B CRC64;

Query Match 15.7%; Score 357; DB 5; Length 286;  
Best Local Similarity 36.1%; Pred. No. 5.4e-23;  
Matches 83; Conservative 37; Mismatches 78; Indels 32; Gaps 4;  
AY 164 DIVAIMIGNLKGTKILQSGIQGVIMVEVGRKKHGW...NHSIFFVSVSFFIITAA 220  
b 14 NAAVITYQNGQLSLTDKGVNIIISIEGRGVRTISLNR...SVLFSISFIVLMII 73  
JY 221 TVGVFIYFAPLPNAPQAQRKORQKADAKKAIGKQLRLTKQDKEIGPDGSCAVCI 280  
b 74 SLVWLIIFYIQRFPYMOAQDQSSNLCVTKKAIKIPTKTGFSO-EKDLSDCAICI 132  
JY 281 ELYKPNLVRILCNHIFKTCVDPWLEHRTCPMKCDILKALG... 325  
b 133 EAYKPTDITIRLPCKHGFHNKIDPWLIEHRTCPMKDLVLFYGVVGVQIVQTPSQH 192  
JY 326 -----IEVDVDEGVSLSQ-VPVSNASNTASPHEDSRSTAS 362  
b 193 TAPTASIEVPVIVVAVPHGPPQLQASNMSSFAFVFSRSPSS 242

Sequence  
B  
2

RESULT 7  
ID O76671 PRELIMINARY; PRT: 473 AA.  
AC O76671;  
DT 01-NOV-1998 (Tremblrel. 08, Created)  
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE H10E21.5 PROTEIN.  
GN H10E21.5  
OS Caenorhabditis elegans  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,  
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fulton L.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,  
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnson L.,  
RA Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P.,  
RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,  
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,  
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Vaughan K., Waterston R.,  
RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,  
RT \*2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans\*;  
RL Nature 368:32-38(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RC Davidson S., Wohlmann P., Courtney L.,  
RT \*The sequence of C. elegans cosmid H10E21\*;  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RC Waterston R.,  
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
CC - SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.  
LR EMBL: AF078783; AAC26923.1;  
DR InterPro: IPR001841;  
DR InterPro: IPR003015;  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.  
DR SMART: SM00184; RING; 1.  
DR Zinc-finger.  
SQ SEQUENCE 473 AA; 52868 MW; 498647C8B56E0957 CRC64;

Query Match 14.5%; Score 329; DB 5; Length 473;  
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Matches 70; Conservative 45; Mismatches 73; Indels 20; Gaps 4;  
QY 206 SIFFVSVSFFIITAAVTVGYFIPYSARRLNARQAQRKORQKADAKKAIGKQLRLTKQ 265  
b 159 SVLFVSISFIIILMW:SLAWLFVYVQPFYAHAKDPLQRLFNARAKAULTRIPTMTIPG 218  
QY 266 -DKEIGPDGDSCAVCIELYKPNLVRILCNHIFKTCVDPWLEHRTCPMKCDILKAL 324  
b 219 MTQELQSD---CAVCLDPYQLQDVIRLLPCKHLYKSCIDPWLIEHRTCPMKNDILKHF 275  
QY 325 GIEVDV-----EDGVSLSQVPVSNASNTASPHEDSRSTASPHGVASVQ 370  
b 276 GYWNDRINDIOPTNSRGADDFITRLEGEHQAPSADVISPEANSNTSDSGSFSDN 335  
QY 371 ADEPPLLEHAQSANML--OLYNHEANS 396  
b 336 SEHHHSEFSGYGTSTVPFQVLNASNA 363

RESULT 8  
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AC O54965;  
DT 01-JUN-1998 (Tremblrel. 06, Created)  
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE RING ZINC FINGER PROTEIN.  
GN RZF.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Lomax M.I., Warner S.J., Bersiril C.G., Gong T.-W.L.;  
RL Prim. Sens. Neuron 0:0-0(1998).  
CC - SIMILARITY: CONTAINS A RING (C3HC4-CLASS) ZINC FINGER.  
DR EMBL: AF037205; AAC03770.1;  
DR InterPro: IPR000561;  
DR InterPro: IPR001841;  
DR InterPro: IPR003137;  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR Pfam: PF02225; PA; 1.  
DR PROSITE: PS01186; EGF\_2; UNKNOWN\_1.  
DR